

Sequence Alignment #2

<!--StartFragment-->RESULT 2

TSHB_CANFA

ID TSHB_CANFA Reviewed; 138 AA.
AC P54828;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 24-JUL-2007, entry version 40.
DE Thyrotropin subunit beta precursor (Thyroid-stimulating hormone
DE subunit beta) (TSH-beta) (TSH-B) (Thyrotropin beta chain).
GN Name=TSHB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Pituitary;
RA Kania S.A., Frank L.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Indispensable for the control of thyroid structure and
CC metabolism.
CC -!- SUBUNIT: Heterodimer of a common alpha chain and a unique beta
CC chain which confers biological specificity to thyrotropin,
CC lutropin, follitropin and gonadotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glycoprotein hormones subunit beta
CC family.
CC -----
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CC -----
DR EMBL; U51644; AAA97410.1; -; mRNA.
DR UniGene; Cfa.3841; -.
DR HSSP; P01233; IHCN.
DR Ensembl; ENSCAFG0000009713; Canis familiaris.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR PANTHER; PTHR11515; Gly_hormoneB; 1.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GH3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
PE 2: Evidence at transcript level;
KW Glycoprotein; Hormone; Secreted; Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 132 Thyrotropin subunit beta.
FT /FTId=PRO_0000011742.
FT PROPEP 133 138 By similarity.
FT /FTId=PRO_0000011743.
FT CARBOHYD 43 43 N-linked (GlcNAc . . .) (Potential).
FT DISULFID 22 72 By similarity.
FT DISULFID 36 87 By similarity.
FT DISULFID 39 125 By similarity.
FT DISULFID 47 103 By similarity.
FT DISULFID 51 105 By similarity.
FT DISULFID 108 115 By similarity.
SQ SEQUENCE 138 AA; 15666 MW; A3298FFDDF6A005F CRC64;

Query Match	94.5%	Score	728	DB	1	Length	138		
Best Local Similarity	94.9%	Pred. No.	5.7e-65						
Matches	131	Conservative	2	Mismatches	5	Indels	0	Gaps	0

Qy 1 MTAIYLSVLFGLAGCQAMSFCFPTEYMMHVERKECAYCLTINTTICAGYCMTRDINGKL 60
||| ||||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MTAIYLSMLMFLGACGQAMSFCFPTEYTMHVERKECAYCLTINTTICAGYCMTRDINGKL 60

Qy 61 FLPKYALSDQDVCTYRDFLYKTVEIPGCPCHVTPYFSYPVAVSKCGKCNTDYSDCIHEAI 120
||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FLPKYALSDQDVCTYRDFMYKTVEIPGCPRHVTYFSYPVAVSKCGKCNTDYSDCIHEAI 120

Qy 121 KTNDCTKPKQSDVVGVSI 138
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Db 121 KTNYCTKPKQSYVVGFSI 138

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